

FIG. 1A-1

Signal peptide

MMP-1 MHSEPPLLLLFWG-----VVSHSEF-----ATLETQ
 MMP-2 MEALMARGALTGPLRALCLLGCLLSHAA-----AP-----SPIIKFPG
 MMP-3 MKSLPILLLLCVAV-----CSAYP-----LDGAARGE
 MMP-7 MR-LTVLCVCLL-----PGSLALP-----LPQE
 MMP-8 MFSLKTLPFLLLLH-----VQISKAFP-----VSSK
 MMP-9 MSLWQPLVLLVLGCG-----FAAPRQRQSTLVLFPG
 MMP-10 MMHLAFVLLCLPV-----CSAYP-----LSGAAKEE
 MMP-11 MAPAAWLRSAARALLPPMLLLQLPPPLARALP-----
 MMP-12 MKFLLILLQ-ATA-----SGALP-----LNSSTSLE
 MT-MMP-1 MSPAPRPSRCLLPLLTGLTALASLGSAQSSSEF-----
 MT-MMP-3 MILLTFSTGRRLDFVH-----HSGVFFLQTLWLILCATVCG
 Consensus M..L..L...L..-----A.P-----.....

Pro-peptide

MMP-1 DAETLKVMKQPRCGVPDVAQ-----FVLTEGNPRWEQTHLT
 MMP-2 DQNTIETMRKPRCGNPDVAN-----YNFFPRKP KWDKNQIT
 MMP-3 DSDTLEVMRKPRCGVPDVGH-----FRTFPGIP KWRKTHLT
 MMP-7 NSRVIEIMQKPRCGVPDVAE-----YSLFPNSPKWTSKVVT
 MMP-8 NEETLDMKKKPRCGVPDSSG-----FMLTPGNPKWERTNLT
 MMP-9 DSATLKAMRTPRCGVPLDGR-----FQTFEGDLKWHHHNIT
 MMP-10 DTDTEVMRKPRCGVPDVGH-----FSSFPGMP KWRKTHLT
 MMP-11 APRPASSLRPPRCGVDPDPSD-GLSARNRQKREVLSSG--RWEKTDLT
 MMP-12 DTSTLEMMHAPRCGVPLDLH-----FREMPGGPVWRKHYIT
 MT-MMP-1 DADTMKAMRRPRCGVPDKFGAEIKANVRRKRYAIQ-G-LKWQHNEIT
 MT-MMP-3 DRNTIDWMKKKPRCGVPDQTRGSSKFHIRRKRYALTQ--KWQHKHIT
 Consensus D..TL..MRKPRCGVPD...-----F...PG.PKW.....T

↑ IS-1

FIG. 1A-2

Pro-peptide

EQVDLVQKYLEKYNNLKNDRQVEKRRNSGPVV-EKLKQMQUEFFGLKVTGKP 79
 DVAPK-TDKELAVQYLNTF-YGCPKE-SCNLFVLKDTLKKMQKFFGLPQTGDL 89
 DTSMLVQKYLENYDLKDVVKQFVRRKDSGPVV-KKIREMQKFFGLGLEVTKGL 79
 AGMSELQWEQAQDY-LKRFYLYDSETKNANSLE-AKLKEMQKFFGLPITGML 74
 EKNTKTVDYLEKFYQLPSNQYQSTR-KNGTNVIVEKLEKEMQKFFGLNVTGKP 78
 DLRTNLTDRQLAEELYRYGYTRVAEMRGESKSLGPALLLQKQLSLPETGEL 86
 DSNKDLAQYLEKYNNLEKDVKQFRRK-DSNLIV-KKIQGMQKFFGLGLEVTKGL 78
 -----PDVHHLHAERRGPQ-----PWHALPSSPAPATQE 67
 KNNVLFGERYLEKFYGLEINKLPVTMKYSGNLMKEKIQEMQHFLGLKVTGQL 79
 -----EAWLQQYGYLPPGDLRTHTQRSQSLS-AAIAAMQKFFGLQVTGKA 80
 TEQYFNVEVWLQKYGYLPPPTSPRMSVVRSAETMQ-SALAAQQQFYGINMTGKV 88
L...Y.L.....-KL..MQKF.GL.VTGKL 100

Catalytic

YRIENYTPDLPRADVDHAIEKAFQLWSNVTPLTFTKV-----SEQQADIM 160
 YRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRI-----HDGEADIM 170
 YRIVNYTPDLPKDAVDSAVEKALKVWEEVTPLTFSRL-----YEGEADIM 160
 YRIVSYTRDLPHTVDRLVSKALNMWGKEIPLHFRKV-----VWGTADIM 155
 YRIRNYTPQLSEAEVERAIKDAFELWSVASPLIFTRI-----SQGEADIN 159
 YWIONYSEDLPRAVIDDAFARAFALWSAVTPLTFTRV-----YSRDADIV 167
 YRIVNYTPDLPKDAVDSKALVWEEVTPLTFSRL-----YEGEADIM 159
 YRILRFPWQLVQEQVRQTMAEALKVWSDVTPLTFTFV-----HEGRADIM 156
 YRINNYPDMNREDVDYAIRKAFQVWSNVTPPLKFSKI-----NTGMADIL 160
 FCIONYTPKVGEYATYEAIRKAFRVWESATPLRFREVVPYAIREGHEKQADIM 178
 YSIKNVTPKVGDPETRKAIRRAFQVWQNVTPLTFTFEEVPYSELENGK-RDVDIP 185
 YRI.NYTPDL...VD.AI.KAF.VWS.VTPLTF..V-----G.ADIM 200

↑ IS-2

FIG. IB-2

211
 270
 211
 207
 210
 267
 210
 208
 211
 229
 237
 300

211
 369
 211
 207
 210
 367
 210
 208
 211
 229
 237
 400

FIG. 1C-1

	Catalytic	Hinge
MMP-1	-----LHRVAA-HELGHSLGLSHST	-----RSQNP
MMP-2	DGKMWCATTANYDDDRKWGFCPDQGYSLFLVAA-HEFGHAMGLEHSQ	-----ASPDIDLGTG
MMP-3	-----LFLVAA-HEIGHSLGLFHS	-----PPDSPETPLVPT
MMP-7	-----FLYAA-THLGHSLGMGHSS	-----LSSNP
MMP-8	-----LFLVAA-HEFGHSLGLAHSS	APPTVCPTGPPTVHPSERPTAGPTGPPSAGPTGPPTAGPSTA-TTVP
MMP-9	DGRLWCATTSNFSDSKKWGFCPDQGYSLFLVAA-HEFGHALGLDHSS	-----PPASTEELVPTK
MMP-10	-----LFLVAA-HELGHSLGLFHS	-----QPWPTVTSRTPALGPQAGIDTNE
MMP-11	-----LLQVAA-HEFGHVLGLQHTT	-----DPKENQRL
MMP-12	-----LFLTAV-HEIGHSLGLGHSS	-----GESGFPTKMPPQPRRTTSRPSVP
MT-MMP-1	-----GNDIFLVAV-HELGHALGLEHSS	-----SPDKIPPPTRLPTVPPHRSIPPADPRKNDPRKPPRPPT
MT-MMP-3	-----NDLFLVAV-HELGHALGLEHSN	-----
Consensus	-----LFLVAA-HE.GHSLGL.HS.	-----
MMP-1		
MMP-2		
MMP-3		
MMP-7		
MMP-8		
MMP-9		
MMP-10		
MMP-11		
MMP-12		
MT-MMP-1		
MT-MMP-3		
Consensus		

FIG. IC-2

Hinge

DIGALMPSY-TFS--GDVQLAQDD-IDGIAIYG-----261
 DPGALMAPIY-TYT--KNFRLSQDD-IKGIQELYG-----446
 NTEALMPLYHSLDTRFRLSQDD-INGIQSLYG-----264
 DPNVAMYPTYGN-GDPQNFKLSQDD-IKGIQKLYGKRSNRKK-----267
 DPGALMYPNYA-FRETSNYSLPQDD-IDGIAIYG-----262
 VPEALMYPMY-RFTE--GPP LHKDD-VNGIRHLYGPRPEPRPTTTTPQPT462
 NTEALMPLYNSFTELAQFRLSQDD-VNGIQSLYG-----263
 AAKALMSAFYT-FRYPL--SLSPDD-CRGVQHLYG-----258
 DPKAVMFPTYK-YVDINTFRLSADD-IRGIQSLYG-----263
 DPSAIMAPFYQ-WMDTENFVLPDDD-RRGIQQLYG-----284
 DPTAIMAPFYQ-YMEQ-TLQLPDDD-YR-HQ-RYM-----288
 DP.ALMYP.Y.....F.LSQDD-I.GIQ.LYG-----500

Hemopexin

VQPI-GPQTPKACDSKLTFDAITTIRGE-VMFFKDRFYMRTNPFY--PEVELN315
 PTPTLGPVTPEICKQDIVFDGIAQIRGE-IFFFKDRFIWRTVTPRDKPMG-PL507
 PVPP-EPGTPANCDPALSFDVSTLRGE-ILIFKDRHFWRKSLRK--LEPELH327
 -----267
 IQPT-GPSTPKPCDPSLTFDAITTLRGE-ILFFKDRYFWRRHQPQL--QRVEMN316
 LSPVDD-----ACN-VNIFDAIAEI-GNQLYLFKDGKYWRFSEGRSRPQGP554
 SVPS-GSEMPAKCDPALSFDASTLRGE-YLFFKDRYFWRRSHWN-PEPEFH326
 IAPLEPDAPPDACE--ASFDAVSTIRGE-LFFFKAGFVWRLRGGL-QPGYPA330
 PNPD--NSEPALCDPNLSFDVAVTTV-GNKIFFFKDRFFWLKVSRP-KTSVN-319
 DKPKNPTYGPNICD--GNFDTVAMLRGEMFVFKK-RWFWRVRNQNQMDGYPM-355
 GRPSYPGAKPNICD--GNFNTLAILRREMVF-KDQWFWRVRNNRV-MDGYPM376
 ..P.-....P...CD....FDA..T.RGE-.FFKDR.FWR.....-.....600

FIG. ID-1

	Hemopexin
MMP-1	FTSVFWPQLPNGLEAAVEFADRDEVRFKGNKYWAV-QGQNVLHGYPKDIYSSFGEPR
MMP-2	LVATEWPELPEKIDAVYEAPQEEKAVFFAGNEYWIY-SASTLERGYPKPLTS-LGLPP
MMP-3	LISFVPSLPSGVDAAYEVTSKDLVFIKGNQFWAI-RGNEVRAGYPRGIHT-LGFPP
MMP-7	-----
MMP-8	FISLFWPSLPTGIQAAYEDEFDRDLIFLFGKNQYWAL-SGYDILQGYPKDISN-YGFPS
MMP-9	LIADKWPALPRKLDVSFEELSKKLFFFSGRQVWVYTGASVL--G-PRRLDK-LGLGA
MMP-10	LISAFWPSLPSYLDAAVEVNSRDTVFIKGNQFWAI-RGNEVQAGYPRGIHT-LGFPP
MMP-11	LASRHWQGLPSPVDAAFE-DAQGHIWFFQGAQYWVY-DGEKPVLG-PAPLTE-LGLVR
MMP-12	LISSLWPTLPSGIEAAVEIARNQVFLFKDDKYWLI-SNLRPEPNYPKSIHS-FGFNP
MT-MMP-1	PIGQFWRGLPASINTAYERKDGKEVF-FKGDKHWF-DEASLEPGYPKHIKE-LGRGL
MT-MMP-3	QITYFWRGLPSPIDAVYENS DGNFVF-FKGNKYWVF-KDTTLQPGYPHDLIT-LGSGI
Consensus	LIS.FWP.LP...DAAYE.....VF.FKGN.YW...-.....GYP..I...-LG.P.

	Hemopexin
MMP-1	MI AHDFPGIGHKVDAVFMKDGFF--YFFHGTQYKFDEPKT-KRILTL-QKANS-WFNC
MMP-2	LIADAWNAI PDNLDAVVDLQGGGHSYFFK GAYY LKLENQS-LKSVKF-GSIKSDWLGC
MMP-3	QIAEDFP GIDSKIDAVFEEFGFF--YFFT GSSQLEFDPNA-KKVTHT-LKSNS-WLNC
MMP-7	-----
MMP-8	SISGAFFGIESKVDAVFQQEHFF--HVFSGPRYYAFDLIA-QRVTRV-ARGNK-WLNC
MMP-9	EVDRMFPGVPLDTHDVFQYREKA--YFCQDRFYWRVSSRSELNQVDQVGVTYDILQC
MMP-10	LIADDFPGVEPKVDVAVLQAFGFF--YFFSGSSQFEFDPNA-RMVTHI-LKSNS-WLHC
MMP-11	R-ATDWRGVPS EIDAAFQDADGYA-YFLRGRLYWKFEDEVK-VKALEGFPLVGPDEFFG
MMP-12	LITKNFQIGIPKIDAVFYSKNKY--YFFQGSNQFEYDELL-QRITKT-LKSNS-WFGC
MT-MMP-1	NIKVWE-GIPESPRGFMGSDVFTYFYKGNKYWKFNQKLKVEPGYPKSA LRDMGC
MT-MMP-3	PITVWK-GIPES PQAFVHKENGFTYFYKEGVLEIQITRYSRLEPGHPR SILKDLSCC
Consensus	.I...F.GI....DAVF.....--YFF.G.....FD....-.....-W...C

FIG. ID-2

TVKHIDAA-LSEENTGKTYFFVANKYWRYDEYKRSMDPGYPK	413
DVQRVDAA-FNWSKNKTTYIFAGDKFWRYNEVKKKMDPGFPK	604
TVRKIDAA-ISDKEKNKTYFFVEDKYWRFEDEKRNSMEPGFPK	424
-----	267
SVQAIDAA-VFYRS--KTYFFVNDQFWRYDNQRQFMEPGYPK	411
DVAQVTGA-LRSGR-GKMLLESGRRLLWRFDVKAQMVDPRSAS	648
TIRKIDAA-VSDKEKKKTYFFAADKYWRFEDENSQSMEQGFPR	423
FP--VHAALVWGPEKNKIYFFRGRDYWRFHPSSTRRVDSPVPR	424
FVKKIDAA-VFNPRFYRTYFFVDNQYWRYDERRRQMDPGYPK	416
PTDKIDAA-LFWMPNGKTYFFRGNKYRNFNEELRAVDSEYPK	451
PPHGIDSA-IWVEDVGKTYFFKGDYRWRYSEEMKTMDPGYPK	472
.V..IDAA-.....KTYFF....YWR.DE....MDPG.PK	700

RKN-----	469
-----	660
-----	477
-----	267
RYG-----	467
PED-----	707
-----	476
CAEPANTFL-----	488
-----	470
PSGGRPDEGTEETE-VIIIEVDEEGGAVSAAAVLPVLLL	549
DGPTDRVKEGHSPPDDVDIVIKLDNTASTVKAIAIVIPCILA	571
-----	800

FIG. 1E

MMP-1	----	469
MMP-2	----	660
MMP-3	----	477
MMP-7	----	267
MMP-8	----	468
MMP-9	----	708
MMP-10	----	476
MMP-11	----	489
MMP-12	----	470
MT-MMP-1	LLVLAVGLAVFFRRHGTPTRRLLYCQRSLDKV	582
MT-MMP-3	LCLLVLVYTVFQFKRKGTPTRHILYCKRSMQEWV	604
Consensus	-----	833

FIG. 2

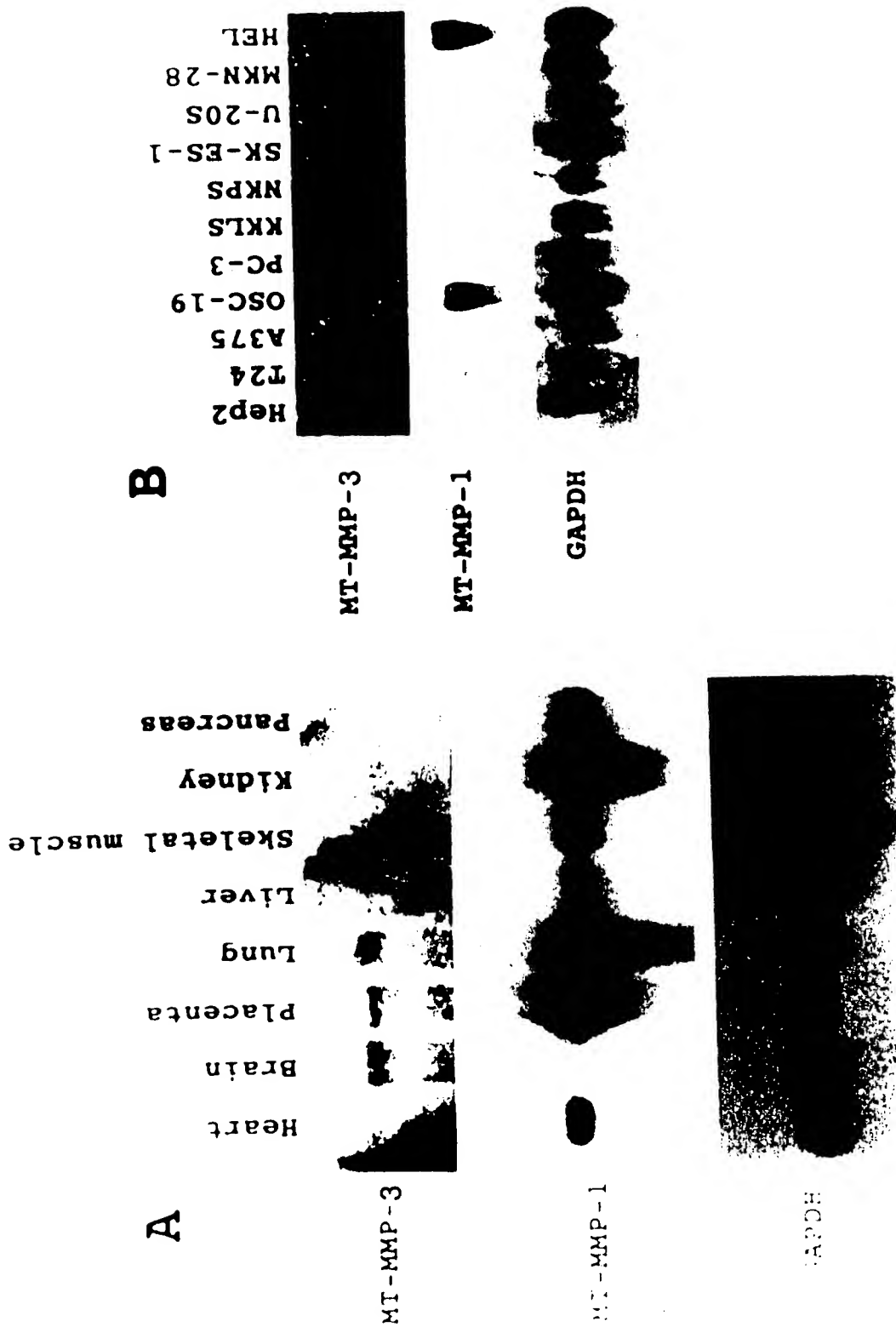
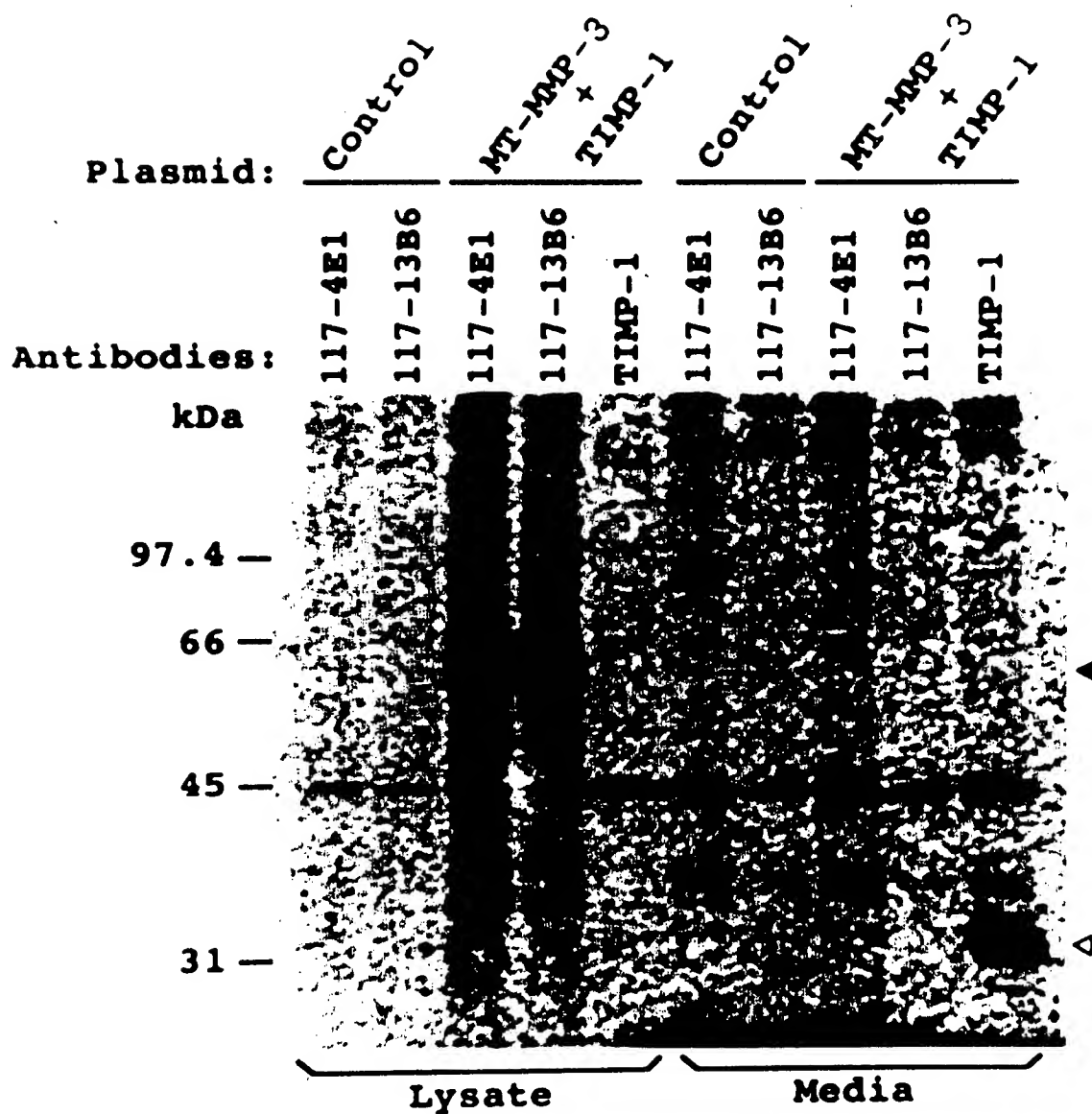
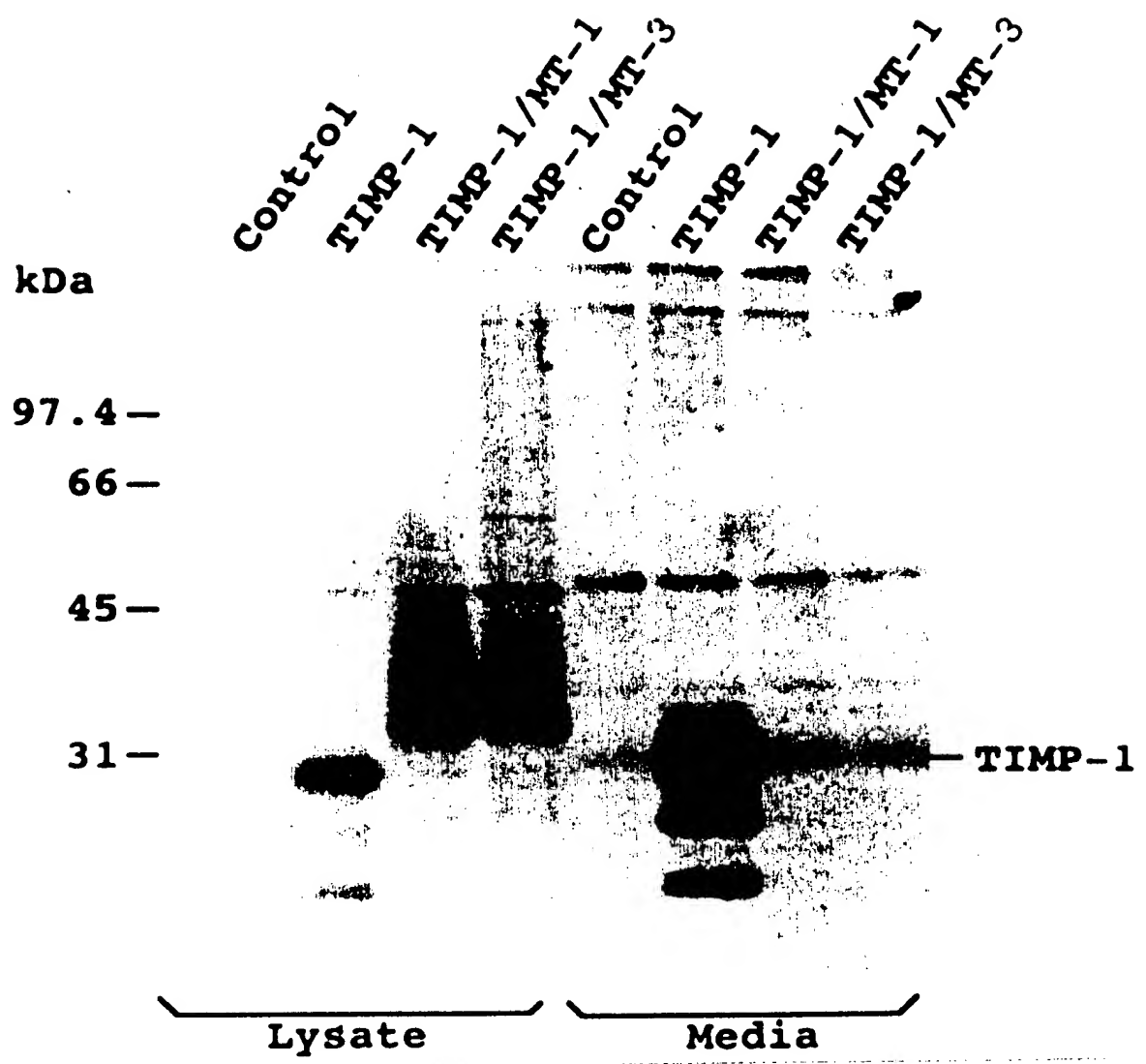


FIG. 3



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FIG. 4



TIMP-1/MT-3



FIG. 6

